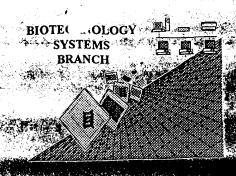
Yord

## RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information?

Genter (STIC) detected errors when processing the following computer readables form:

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

2) STELEPHONING APPLICANT AND FAXING A COPYOF THIS PRINTOUT WITH A SENOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308 PATENTIN 2.1 e-mail help: \*patin21help@uspto.gov or phone 703-306-4119 (R. Wax) PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

## **Checker Version 3.0**

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K<sup>2</sup> compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

http://www.uspto.gov/web/offices/pac/checker

SERIAL NUMBER: 09/

## ERROR DETECTED SUGGESTED CORRECTION

ATTN	: NEW RULES CASES:	PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE
1	Wrapped Nucleics	The number/text at the end of each line "wrapped" down to the next line.
		This may occur if your file was retrieved in a word processor after creating it.
		Please adjust your right margin to .3, as this will prevent "wrapping".
2	Wrapped Aminos	The amino acid number/text at the end of each line "wrapped" down to the next line.
		This may occur if your file was retrieved in a word processor after creating it.
		Please adjust your right margin to .3, as this will prevent "wrapping".
3	Incorrect Line Length	The rules require that a line not exceed 72 characters in length. This includes spaces.
4	Misaligned Amino Acid	The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
	Numbering	between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
5	Non-ASCII .	This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
	•	Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
6	Variable Length	Sequence(s) contain n's or Xaa's which represented more than one residue
<u> </u>	· variable congri	As per the rules, each n or Xaa can only represent a single residue.
		Please present the maximum number of each residue having variable length and
		indicate in the (ix) feature section that some may be missing.
7	Patentin ver. 2.0 "bug"	A "bug" in Patentln version 2.0 has caused the <220>-<223> section to be missing from amino acid
		sequence(s)
		previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
	•	to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
		sections for Artificial or Unknown sequences.
8	Skipped Sequences	Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
	(OLD RULES)	(2) INFORMATION FOR SEQ ID NO:X:
		(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
		(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
		This sequence is intentionally skipped
		Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
9	Skipped Sequences	Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
	(NEW RULES)	<210> sequence id number
		<400> sequence id number
		000
0	Use of n's or Xaa's	Use of n's and/or Xaa's have been detected in the Sequence Listing.
	(NEW RULES).	Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
		In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
1	Use of <213>Organism	Sequence(s) are missing this mandatory field or its response.
ſ	(NEW RULES)	2 M
/	**	27
2 —	Use of <220>Feature	Sequence(s) are missing the <220>Feature and associated headings.
	(NEW RULES)	Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
		Please explain source of genetic material in <220> to <223> section.  (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
		(See reuelal Register, 0/01/30, Vol. 03, 140, 104, pp. 23031-32) (Sec. 1.823 of new Rules)
3	Patentin ver. 2.0 "bug"	Please do not use "Copy to Disk" function of Patentin version 2.0. This causes a corrupted
		file, Tesalting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).

Instead, please use "File Manager" or any other means to copy file to floppy disk.

RAW SEQUENCE LISTING DATE: 03/08/2001 PATENT APPLICATION: US/09/619,047 TIME: 14:25:01

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Output Set: N:\CRF3\03082001\I619047.raw

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    32 Gly Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val Leu Asp Ser
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    39 ttt tta cat ggt aac gcg gcc tct tct tat tta tgg cga cat gtt gtg
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    40 Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg His Val Val
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                                                     60
    43 cca cat att gag cca gta gcg cgg tgt att ata cca gat ctt att ggt
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    44 Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp Leu Ile Gly
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    47 atg ggc aaa tca ggc aaa tct ggt aat ggt tct tat agg tta ctt gat
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    52 His Tyr Lys Tyr Leu Thr Ala Trp Phe Glu Leu Leu Asn Leu Pro Lys
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                                       105
    55 aag atc att ttt gtc ggc cat gat tgg ggt gct tgt ttg gca ttt cat
    56 Lys Ile Ile Phe Val Gly His Asp Trp Gly Ala Cys Leu Ala Phe His
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                                   120
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    60 Tyr Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val His Ala Glu
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    63 agt gta gta gat gtg att gaa tca tgg gat gaa tgg cct gat att gaa
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    64 Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro Asp Ile Glu
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DATE: 03/08/2001 TIME: 14:25:01 RAW SEQUENCE LISTING PATENT APPLICATION: US/09/619,047

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73 180 185 190 .	
75 aag tta gaa cca gaa gaa ttt gca gca tat ctt gaa cca ttc aaa gag	624
76 Lys Leu Glu Pro Glu Glu Phe Ala Ala Tyr Leu Glu Pro Phe Lys Glu 77 195 200 205	
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96 Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His Phe Ser Gln	
97 275 · 280 285	
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101 290 295 300	
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	C1		7	Db -		37 a 1	G1	m la sa	M-+		Desc	C	T	т1.		7 ~~ ~~	
	GIU	ASII	ASII		Phe	Val	GIU	THE		Leu	Pro	ser	ьуѕ		met	AIG	
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151	Gru	290	мта	FIO	иэр	GIU	295	GTÅ	пĵэ	тут	116	300	Ser	FILE	Val	Giu	
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DATE: 03/08/2001 RAW SEQUENCE LISTING PATENT APPLICATION: US/09/619,047 TIME: 14:25:01

Input Set : A:\sequence
Output Set: N:\CRF3\03082001\I619047.raw

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189	Mec	GIY	ьуѕ	ser	85	гаг	ser	GIĀ	ASN	Gly 90	ser	туг	Arg	Leu	ьеи 95	Asp	
	ant.	+ > 0	222	+ - +		20+	~~~	taa	+++		a++	a++	t	++-		226	336
							_			gaa, Glu						_	220
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	224	2 + 2	~++		~ 1- ~	~~~	aa t	~ ~ +			~~+	++	++~		4 4 4	aa+	384
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	тÀг	116		Pne	Val	GIÀ	nis		ттр	Gly	Ald	Cys		Ald	Pne	HIS	
197			115				~~+	120					125				422
		_					_	_		aaa	•		-		_	-	432
	TÀ L	130	TAL	GIU	HIS	GIII	135	гàг	me	Lys	Ala		val	HIS	Ala	GIU	
201	t								<b>.</b>			140					400
										gat							480
		val	vai	ASP	val		GIU	ser	тгр	Asp		тгр	Pro	ASP	TTe		
	145					150					155					160	F 2 0
	-	-			_				-	gaa		-		_	-	_	528
	GIU	ASP	ile	Ala		11e	Lys	ser	Glu	Glu	ĠΤĀ	GIU	ьуs	мет		Leu	
209					165					170		4			175		E76
							-		_	ttg					•	-	576
	GLU	ASII	ASI		Pne	vai	GIU	THE		Leu	Pro	ser	гÀг		мес	Arg	
213			~~~	180				~~~	185				~~~	190		~~~	624
	-				-	-	-	_	_	tat		_					624
	гÀг	Leu		Pro	ASP	GIU	val	_	Ата	Tyr	ьeu	GIU		Phe	гуѕ	GIU	
217		~~+	195	~++	~~+	~~+		200	Helen		+ ~ ~	~~+	205	~~~	-+-		673
			-	-	-	_				tca			-	-		_	672
	гуѕ	210	GIU	Val	AIG	Arg	215	THE	Leu	Ser	тгр		AIG	GIU	TTe	PIO	
221	++-		222	~~+	~~+	222		~~~	~++	a+ 5		220	~++	200	2 2 t	+ - +	720
		_						_	-	gta			-				120
	225	val	тλг	СТУ.	GIY	230	PIO	ASP	Val	Val	235	116	val	AIG	ASII	240	•
		a a t	+ - +	a+ a	aat		2 at	ant.	~ a +	tta		222	2 + 0	+++	~++		768
						_	_	-	-	Leu			_			_	700
229	ASII	AId	тут.	пеп	245	ніа	sei	мэр	MSP	250	PIO.	цу́з	Met	rne	255	Giu	
	+ ca	a +	.002	aas		+++	+ 00	22t	act	att	at t	(T = 2	aac	acc		224	816
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233	261	кэр	FIO	260	FIIE	rne	261	ASII	265	116	vaı	GIU	GIY	270	пұз	пуз	
	+++	act	aat		as a	+++	ata	222		aaa	aat	ctt	cat		tca	C22	864
					-		_		-	Lys					-		004
237	rne	110	275	1111	GIU	FILE	val	280	Val	цур	GLY	пец	285	rne	Jer .	GIII	
	gaa	αat		cct	gat	gaa	ata		aaa	tat	atc	aaa		ttc	att	gag	912
	-	-	-		-	-	_			Tyr			_		_		
241	Olu	290	niu	110	лэр	Olu	295	OLY	Dy 3	1 7 1	110	300		1110	val	Gru	•
	cga		ctc	aaa	aat	gaa	-	taa				300					936
	-	-				Glu		cuu									230
245		,		ביים		310	0111										
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	<212																
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RAW SEQUENCE LISTING DATE: 03/08/2001 PATENT APPLICATION: US/09/619,047. TIME: 14:25:01

Input Set : A:\sequence

Output Set: N:\CRF3\03082001\1619047.raw

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                                 40
260 Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg His Val Val
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262 Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp Leu Ile Gly
263 65
                         70
264 Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg Leu Leu Asp
266 His Tyr Lys Tyr Leu Thr Ala Trp Phe Glu Leu Leu Asn Leu Pro Lys
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                                    105
                                                        110
268 Lys Ile Ile Phe Val Gly His Asp Trp Gly Ala Cys Leu Ala Phe His
           115
                                120
270 Tyr Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val His Ala Glu
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                            135
272 Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro Asp Ile Glu
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                                            155
274 Glu Asp Ile Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys Met Val Leu
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                                        170
                                                            175
276 Glu Asn Asn Phe Phe Val Glu Thr Met Leu Pro Ser Lys Ile Met Arg
277
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                                    185
278 Lys Leu Glu Pro Asp Glu Val Asp Ala Tyr Leu Glu Pro Phe Lys Glu
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280 Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg Glu Ile Pro
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282 Leu Val Lys Gly Gly Lys Pro Asp Val Val Gln Ile Val Arg Asn Tyr
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284 Asn Ala Tyr Leu Arg Ala Ser Asp Asp Leu Pro Lys Met Phe Ile Glu
                    245
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286 Ser Asp Pro Gly Phe Phe Ser Asn Ala Ile Val Glu Gly Ala Lys Lys
                260
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288 Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His Phe Ser Gln
          275
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290 Glu Asp Ala Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser Phe Val Glu
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292 Arg Val Leu Lys Asn Glu Gln
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306 <400> SEQUENCE: 5
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<211> 8
<212> PRT
<213 Artificial Sequence sel tem /2 on Evan Summary Sheet
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Arg Pro Leu Gly Ile Ile Gly Gly

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FYI

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/619,047

DATE: 03/08/2001 TIME: 14:25:02

Input Set : A:\sequence

Output Set: N:\CRF3\03082001\I619047.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date L:551 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:22 L:551 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:22 L:551 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:22 L:568 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:23 L:568 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:23 L:568 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:23 L:613 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:26 L:613 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:26 L:613 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:26 L:622 M:258 W: Mandatory Feature missing, <220> FEATURE: L:622 M:258 W: Mandatory Feature missing, <220> FEATURE: L:622 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: